

DT 01-OCT-2000 (TREMURel_15, last annotation update)
DE VICTILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
OS Juglans regia (English walnut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Rgales; Juglandaceae; Juglans.
NCBI_TaxID=51240;
(1) _____
RN SEQUENCE FROM N.A.
RP STRAIN=CV_SUNLAND; TISSUE=SOMATIC EMBRYO LINE;
RA Teuber S.S., Jarvis K.C., Peterson W.R., Bandekar A.M., Ansari A.A.;
RC Identification and cloning of a cDNA encoding a vicillin-like protein
RT Jug r 2, from English walnut kernel (Juglans regia) as a major food
RT allergen.
RL Submitted (MAY-1998) to the EMBL/genbank/DBJ databases.
RU EMBL; AF060605; AF018269.1; -.
DR HSSP; P02853; 2PHL.
DR INTERPRO; IPRO001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
DR NON-ref

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Query Match      45.2%;   Score 112;   DB 10;   Length 533;
Best Local Similarity 48.8%;   Pred. No. 8.4e-06;
Matches 20; Conservative 7; Mismatches 14; Indels 0; Gaps 0
2Y      1 NQEDPQTECQCQCQRRCQESDPDQDQYCCRRCKEICEEE 41

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	RESULT	5	
ID	043358	PRELIMINARY;	PRT; 525 AA.
AC	043358:		
DT	01-NOV-1996	(TREMBLrel. 01,	Created)
DT	01-NOV-1996	(TREMBLrel. 01,	Last sequence update)
DT	01-OCT-2000	(TREMBLrel. 15,	Last annotation update)
DE	VICLIN PRECURSOR.		
GN	CSV.		
OS	Theobroma cacao (Cacao).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;		
OC	Malvales; Malvaceae; Theobroma.		
OX	NCBI_TaxId=3641;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LEAVES;		
RX	MEDLINE=92288309; PubMed=1600151;		
RA	McHenry L., Fritz P.J.;		
RT	"Comparison of the structure and nucleotide sequences of vicilin genes		
RT	of cocoa and cotton false questions about vicilin evolution.";		
RL	Plant Mol. Biol. 18:1173-1176(1992).		
EMBL	X62625; CAA44493.1; -		
DB			

RT	of cocoa and cotton structure and nucleotide sequences of vicillin genes			
RL	Plant Mol Biol 18:1173-1176(1992).			
DR	EMBL:	X62625:	CAA44493.1:	-
DR	EMBL:	X62626:	CAA44494.1:	-
DR	HSSP:	P02853:	2PHT.	
DR	MENDEL:	30919:	Thecc::1188:	30919.
DR	INTERPRO:	IPR001113:	-	
DR	PFAM:	PF00546:	Seedstore_7s:	1.
DR	PRODOM:	PD081059:	-:	1.
KW	Signal.			
FT	SIGNAL			
FT	CHAIN	1	24	POTENTIAL.
FT	CHAIN	25	525	VICILIN.
SO	SEQUENCE	525 AA:	60798 MW:	19114CD5C248905D CRC64;
Query Match				
Best Local Similarity	44.48:	Score 110:	DB 10:	Length 525;
Matches 19:	Conservative 10:	Mismatches 11:	Indels	0:
Gaps				0:

Query Match 31.0%; Score 77; DB 5; Length 1513;
Best Local Similarity 43.6%; Pred. No. 0.24;
Matches 17; Conservative 2; Mismatches 16; Indels 4; Gaps 2

OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Dudin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Luthington J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Showkeen R.,
RA Shaldon N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierley-Wieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*
RT elegans".
RL Nature 368:32-38(1994).
RP [2]
RN SEQUENCE FROM N.A.
RP

RC STRAIN-BRISTOL N2;
RA Greco T., Bradshaw H., Elliott G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF016451; AAB66001.1; -
SQ SEQUENCE 388 AA; 42139 MW; 2E20655B099AE92 CRC64;

Query Match 30.2%; Score 75; DB 5; Length 388;
Best Local Similarity 37.5%; Pred. No. 0.13;
Matches 15; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

OY 2 QEDPOTEC-QCCORRCQDESPPRO-QQYQCRKCEEC 39
DB 194 QACQPCQCCQCCSCVQDQDQNSNCEPACNCTCSDICQ 233

RESULT 13
ID 016501 PRELIMINARY; PRT; 388 AA.
AC 016501;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C03A7.7 PROTEIN.
GN C03A7.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RT Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Greco T., Bradshaw H., Elliott G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF016451; AAB65996.1; -
SQ SEQUENCE 388 AA; 42129 MW; 7AAC3953E0AF2A2 CRC64;

Query Match 30.2%; Score 75; DB 5; Length 388;
Best Local Similarity 37.5%; Pred. No. 0.13;
Matches 15; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

OY 2 QEDPOTEC-QCCORRCQDESPPRO-QQYQCRKCEEC 39
DB 194 QACQPCQCCQCCSCVQDQDQNSNCEPACNCTCSDICQ 233

RESULT 14
ID 044606 PRELIMINARY; PRT; 388 AA.
AC 044606;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE R09B5.5 PROTEIN.
GN R09B5.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RT Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Sammons L., Wohlmann P., Bauer C., Antoniou B., Wilson R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF039046; AAB94214.1; -
SQ SEQUENCE 388 AA; 41440 MW; EA9C34AA4EABFE46 CRC64;

Query Match 30.2%; Score 75; DB 5; Length 388;
Best Local Similarity 22.2%; Pred. No. 0.13;
Matches 14; Conservative 15; Mismatches 12; Indels 22; Gaps 2;

OY 2 QEDPOTEC-QCCORRCQ-----QSDPQQQYQCRKCEEC 39
DB 147 QQQPASCQPCQCCQCCNVACDAPATSTQAPQVYHOLEIQDAGQCCQCCQCCSSCTQ 206

OY 40 EEE 42
DB 207 QQQ 209

RESULT 15
ID 016502 PRELIMINARY; PRT; 438 AA.
AC 016502;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C03A7.8 PROTEIN.
GN C03A7.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.

